

PCT

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/786,442 DATE: 03/23/2001  
 TIME: 09:45:58

Input Set : A:\991043sequence.txt  
 Output Set: N:\CRF3\03232001\I786442.raw

**ENTERED**

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3 <110> APPLICANT: ASahi KASEI KABUSHIKI KAISHA
4   TAKAHASHI, Tsuneo
5   ONO, Mitsuharu
6   ISHIMARU, Hiroshi
7   KANNO, Kimiyoshi
8   TAKAHASHI, Chiaki
10 <120> TITLE OF INVENTION: Novel receptor protein and method for the diagnosis of an
11   inflammatory disease by using the same
13 <130> FILE REFERENCE: 99-1043
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/786,442
C--> 15 <141> CURRENT FILING DATE: 2001-03-05
15 <150> PRIOR APPLICATION NUMBER: JP 10-249752
16 <151> PRIOR FILING DATE: 1998-09-03
18 <150> PRIOR APPLICATION NUMBER: JP 11-070800
19 <151> PRIOR FILING DATE: 1999-03-16
21 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04801
22 <151> PRIOR FILING DATE: 1999-09-03
24 <160> NUMBER OF SEQ ID NOS: 12
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1014
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)...(1011)
35 <400> SEQUENCE: 1
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37 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
38   1           5           10           15
39 tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg gcc atc gac      96
40 Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
41   20           25           30
42 ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc ttc ctg gtg     144
43 Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
44   35           40           45
45 ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg aag gtg gcc     192
46 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
47   50           55           60
48 cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc gtg gcg gat     240
49 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
50   65           70           75           80
51 ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc att gcc cgt     288
52 Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
53   85           90           95
54 gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg ctg ccc tcc     336
55 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
56   100          105          110

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57 atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg gca gct ctc 384
58 ile ile leu leu thr met tyr ala ser val leu leu leu ala ala leu
59      115      120      125
60 agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg tgg tct acg 432
61 ser ala asp leu cys phe leu ala leu gly pro ala trp trp ser thr
62      130      135      140
63 gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca gcc tgg aca 480
64 val gln arg ala cys gly val gln val ala cys gly ala ala trp thr
65 145      150      155      160
66 ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc cgg ctg cac 528
67 leu ala leu leu leu thr val pro ser ala ile tyr arg arg leu his
68      165      170      175
69 cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac tac ggc ggc 576
70 gln glu his phe pro ala arg leu gln cys val val asp tyr gly gly
71      180      185      190
72 tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt ctt ttt ggc 624
73 ser ser ser thr glu asn ala val thr ala ile arg phe leu phe gly
74      195      200      205
75 ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt gcc ctc ctg 672
76 phe leu gly pro leu val ala val ala ser cys his ser ala leu leu
77      210      215      220
78 tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc att gtg gtg 720
79 cys trp ala ala arg arg cys arg pro leu gly thr ala ile val val
80 225      230      235      240
81 ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg ctg gtg ctc 768
82 gly phe phe val cys trp ala pro tyr his leu leu gly leu val leu
83      245      250      255
84 act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc ctg cgg gct 816
85 thr val ala ala pro asn ser ala leu leu ala arg ala leu arg ala
86      260      265      270
87 gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc ctc aat ccc 864
88 glu pro leu ile val gly leu ala leu ala his ser cys leu asn pro
89      275      280      285
90 atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg tca ctg cca 912
91 met leu phe leu tyr phe gly arg ala gln leu arg arg ser leu pro
92      290      295      300
93 gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag gac gaa agt 960
94 ala ala cys his trp ala leu arg glu ser gln gly gln asp glu ser
95 305      310      315      320
96 gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg gag atg gag 1008
97 val asp ser lys lys ser thr ser his asp leu val ser glu met glu
98      325      330      335
99 gtg tag 1014
100 val
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 337
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 2

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109 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
110 1 5 10 15
111 Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
112 20 25 30
113 Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
114 35 40 45
115 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
116 50 55 60
117 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
118 65 70 75 80
119 Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
120 85 90 95
121 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
122 100 105 110
123 Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu
124 115 120 125
125 Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
126 130 135 140
127 Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
128 145 150 155 160
129 Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
130 165 170 175
131 Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
132 180 185 190
133 Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
134 195 200 205
135 Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
136 210 215 220
137 Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
138 225 230 235 240
139 Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Gly Leu Val Leu
140 245 250 255
141 Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
142 260 265 270
143 Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
144 275 280 285
145 Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
146 290 295 300
147 Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
148 305 310 315 320
149 Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
150 325 330 335
151 Val
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 1287
156 <212> TYPE: DNA
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 3
160 cctgtgtgcc acgtgctgga caaatcttaa ctctcaagg actcccaaaa ccagagacac 60

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161 caggagcctg aatggggaac gattctgtca gctacgagta tggggattac agcgacctct 120
162 cggaccgccc tgtggactgc ctggatggcg cctgcctggc catcgaccgg ctgcgcgtgg 180
163 ccccgctccc actgtatgcc gccatcttcc tgggtgggggt gccgggcaat gccatgggtg 240
164 cctgggtggc tgggaagggt gccgcggga ggggtgggtgc cactgggtg ctccacctgg 300
165 cgtggcgga tttgtctgtc tgtttgtctc tgcccatcct ggcagtgccc attgcccgtg 360
166 gaggccactg gccgtatggt gcagtgggct gtcgggcgct gccctccatc atcctgctga 420
167 ccatgtatgc cagcgtcctg ctccctggcag ctctcagtgc cgacctctgc ttcctggctc 480
168 tcgggctgct ctggtggtct acggttcacg gggcgtgcgg ggtgcaggtg gcctgtgggg 540
169 cagcctggac actggccttg ctgctcaccg tgccctccgc catctaccgc cggctgcacc 600
170 aggagcactt cccagcccgg ctgcagtgtg tggtagacta cggcggctcc tccagcaccg 660
171 agaatgcggt gactgccatc cggtttcttt ttggcttctt ggggcccctg gtggccgtgg 720
172 ccagctgcca cagtgccttc ctgtgctggg cagcccagcg ctgcggccgg ctgggcacag 780
173 ccattgtggt ggggtttttt gtctgctggg caccctacca cctgctgggg ctggtgctca 840
174 ctgtggcggc ccgaactcc gcaactcctg ccagggccct ggggctgaa cccctcatcg 900
175 tgggccttgc cctcgtcac agctgcctca atcccatgct ctctctgtat tttgggaggg 960
176 ctcaactccg ccggtcactg ccagctgcct gtcactgggc cctgaggggg tcccaggggc 1020
177 aggacgaaag tgtggacagc aagaaatcca ccagccatga cctggtctcg gagatggagg 1080
178 tgtaggctgg agagacattg tgggtgtgta tcttcttatt tctttcaca agactggctt 1140
179 caggcatagc tggatccagg agctcaatga tgtcttcatt ttattccttc cttcattcaa 1200
180 cagatatcca tcatgcactt gctatgtgca aggccttttt aggcactaga gatatagcag 1260
181 tgaccaaacc agacacaaat cctgccc 1287
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 1287
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 4
190 gggcaggatt tgtgtctgtt ttggtcactg ctatatctct agtgccataa aaggccttgc 60
191 acatagcaag tgcattgatg atatctgttg aatgaaggaa ggaataaaat gaagacatca 120
192 ttgagctcct ggtatccagct atgcctgaag ccagctctgt gaaatgagat aagaagatac 180
193 acacccacaa tgtctctcca gctacacct ccatctccga gaccaggtca tggctgggtg 240
194 atttcttctg gtccacactt tctctctggc cctgggactc cctcaggggc cagtgcagg 300
195 cagctggcag tgaccggcgg agttgagccc tcccaaaata cagggaagagc atgggattga 360
196 ggcagctgtg agcgagggca aggccacga tgagggggtc agcccgagg gccctggcca 420
197 ggagtgcgga gttcggggcc gccacagtga gcaccagccc cagcagggtg taggggtccc 480
198 agcagacaaa aaacccacc acaatggctg tgcccagcgg ccggcagcgt cgggctgccc 540
199 agcacaggag ggcactgtgg cagctggcca cggccaccag gggcccagg aagccaaaaa 600
200 gaaaccggat ggcagtcacc gcattctcgg tctgaggga gccgcccgtg tccaccacac 660
201 actgcagccg ggtgggaag tctctctggt gcagccggcg gtagatggcg gagggcacgg 720
202 tgagcagcaa ggcagtgctc caggctgccc caccagccac ctgcacccc cagcccgt 780
203 gaaccgtaga ccaccaggca ggcggagag ccagggaagca gaggtcggca ctgagagctg 840
204 ccaggagcag gacgtggca tacatggtca gcaggatgat ggagggcagc gcccgacagc 900
205 ccaactgcacc atacggccag tggcctccac gggcaatggg cactgcccag atgggcagag 960
206 acaaacagca cagcaaatcc gccacggcca ggtggagcaa ccagggtgga cccacctcc 1020
207 ggcggggcac ctcccccagc acccaggcca ccatggcatt gcccggcacc cccaccagga 1080
208 agatggcggc atacagtgg agcggggcca cgcgcagcgg gtcgatggcc aggcaggcgc 1140
209 catccaggca gtccacaggc cgtccgaga ggtcgtgta atcccatatc tcgtagctga 1200
210 cagaatcggt ccccatcag gctcctgggt tctctggttt tgggagtcct tgaggagtta 1260
211 agatttctcc agcagtggc acacagg 1287
214 <210> SEQ ID NO: 5

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215 <211> LENGTH: 30
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
W--> 220 <221> NAME/KEY: modified base
221 <222> LOCATION: 18
222 <223> OTHER INFORMATION: i
224 <220> FEATURE:
W--> 225 <221> NAME/KEY: modified base
226 <222> LOCATION: 22
227 <223> OTHER INFORMATION: i
229 <220> FEATURE:
W--> 230 <221> NAME/KEY: modified base
231 <222> LOCATION: 24
232 <223> OTHER INFORMATION: i
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Degenerative PCR primer designed based on the seq of conventional
236 7-pass transmembrane receptor proteins which are considered to
237 participate in the proliferation of melanoma
240 <400> SEQUENCE: 5
W--> 241 atcttaagct tgaacctngc cntngcdgac 30
244 <210> SEQ ID NO: 6
245 <211> LENGTH: 33
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
W--> 250 <221> NAME/KEY: misc difference
251 <222> LOCATION: 21
252 <223> OTHER INFORMATION: a, g, c or t
254 <220> FEATURE:
W--> 255 <221> NAME/KEY: modified base
256 <222> LOCATION: 22
257 <223> OTHER INFORMATION: i
259 <220> FEATURE:
W--> 260 <221> NAME/KEY: modified base
261 <222> LOCATION: 28
262 <223> OTHER INFORMATION: i
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Degenerative PCR primer designed based on the seq of conventional
266 7-pass transmembrane receptor proteins which are considered to
267 participate in the proliferation of melanoma
269 <400> SEQUENCE: 6
W--> 270 cccaacgaat tertagatsa nnggrttnav rca 33
273 <210> SEQ ID NO: 7
274 <211> LENGTH: 32
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Synthetic primer used for constructing the recombinant DNA

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VERIFICATION SUMMARY                      DATE: 03/23/2001  
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Input Set : A:\991043sequence.txt  
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L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:220 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:225 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:250 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:255 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:260 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6